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SEQUENCE LISTING

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Metcalf, Donald
Zhang , Jian

<120> A novel haemopoietin receptor and genetic sequences encoding same

<130> 11373

<140> US 09/051843

<141> 1998-06-29

<150> AU PN6135

<151> 1995-10-23

<150> AU PN7276

<151> 1995-12-22

<150> AU PP2208

<151> 1996-09-09

<160> 12

<170> PatentIn version 3.1

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<222> (61)..(1332)

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Met Ala Arg Pro Ala Leu Leu Gly Glu Leu Leu Val Leu Leu Leu Trp
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acc gcc acc gtg ggc caa gtt gcc gcg gcc aca gaa gtt cag cca cct      156
Thr Ala Thr Val Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro Pro
20          25          30
gtg acg aat ttg agc gtc tct gtc gaa aat ctc tgc acg ata ata tgg      204
Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile Trp
35          40          45
acg tgg agt cct cct gaa gga gcc agt cca aat tgc act ctc aga tat      252
Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg Tyr
50          55          60
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cat cgt aaa gag gaa tta ccc ctg gat gag aaa atc tgt ctg cag gtg	348
His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln Val	
85 90 95	
ggc tct cag tgt agt gcc aat gaa agt gag aag cct agc cct ttg gtg	396
Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu Val	
100 105 110	
aaa aag tgc atc tca ccc cct gaa ggt gat cct gag tcc gct gtg act	444
Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val Thr	
115 120 125	
gag ctc aag tgc att tgg cat aac ctg agc tat atg aag tgt tcc tgg	492
Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser Trp	
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Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr Tyr	
145 150 155 160	
tgg tac agc agc ctg gag aaa agt cgt caa tgt gaa aac atc tat aga	588
Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr Arg	
165 170 175	
gaa ggt caa cac att gct tgt tcc ttt aaa ttg act aaa gtg gaa cct	636
Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu Pro	
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Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn Ala Gly	
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Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys Leu Thr	
245 250 255	
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Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn Ile Leu	
260 265 270	
gag gtt gaa gag gac aaa tgc cag aat tcc gaa tct gat aga aac atg	924
Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg Asn Met	
275 280 285	
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Asn	Lys	Leu	Trp	Ser	Asp	Trp	Ser	Glu	Ala	Gln	Ser	Ile	Gly	Lys	Glu		
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gacttttgca	ttgaaaaccc	aaacccaaag	gagctccttc	caagaaaagc	aagagttcct												1542
ctcgttcctt	gttccaatcc	ctaaaagcag	atgttttgcc	aatccccaa	actagaggac												1602
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Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg Tyr
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Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu Thr
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His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln Val
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Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu Val
100 105 110

Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val Thr
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Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser Trp
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Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr Tyr
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Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr Arg
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Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu Pro
180 185 190

Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn Ala Gly
195 200 205

Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr Val Lys
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Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly Ala Leu
225 230 235 240

Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys Leu Thr
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Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn Ile Leu
260 265 270

Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg Asn Met
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Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp Ala Val
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Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly Lys Glu
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Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro Val Phe
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Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg Leu Lys
355 360 365

Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe Lys Glu
370 375 380

Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys Tyr Asp
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gcc ggc ggc ggg ggc ggg ggc ggg ggc gcg cct acg gaa act cag cca	156					
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cct gtg aca aat ttg agt gtc tct gtt gaa aac ctc tgc aca gta ata	204					
Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile						
35 40 45						
tgg aca tgg aat cca ccc gag gga gcc agc tca aat tgt agt cta tgg	252					
Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp						
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tat ttt agt cat ttt ggc gac aaa caa gat aag aaa ata gct ccg gaa	300					
Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu						
65 70 75 80						
act cgt cgt tca ata gaa gta ccc ctg aat gag agg att tgt ctg caa	348					
Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln						
85 90 95						
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Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu						
100 105 110						
gtt gaa aaa tgc atc tca ccc cca gaa ggt gat cct gag tct gct gtg	444					
Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val						
115 120 125						
act gaa ctt caa tgc att tgg cac aac ctg agc tac atg aag tgt tct	492					
Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser						
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Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr						
145 150 155 160						
tat tgg cac aga agc ctg gaa aaa att cat caa tgt gaa aac atc ttt	588					
Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe						
165 170 175						
aga gaa ggc caa tac ttt ggt tgt tcc ttt gat ctg acc aaa gtg aag	636					
Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val Lys						
180 185 190						
gat tcc agt ttt gaa caa cac agt gtc caa ata atg gtc aag gat aat	684					
Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile Met Val Lys Asp Asn						
195 200 205						

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Val Lys Pro Asp Pro Pro His Ile Lys Asn Leu Ser Phe His Asn Asp	
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cta ttt tat gaa gta gaa gtc aat aac agc caa act gag aca cat aat	876
Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln Thr Glu Thr His Asn	
260 265 270	
gtt ttc tac gtc caa gag gct aaa tgt gag aat cca gaa ttt gag aga	924
Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg	
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aat gtg gag aat aca tct tgt ttc atg gtc cct ggt gtt ctt cct gat	972
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act ttg aac aca gtc aga ata aga gtc aaa aca aat aag tta tgc tat	1020
Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr	
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325 330 335	
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Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val Pro	
340 345 350	
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Val Ile Val Ala Gly Ala Ile Ile Val Leu Leu Leu Tyr Leu Lys Arg	
355 360 365	
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Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe	
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385 390 395 400	
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405 410 415	
ctg ata gaa aac ctg aag aaa gcc tct cag tgatggagat aatttatattt	1358
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 35 40 45

Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp
 50 55 60

Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu
 65 70 75 80

Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln
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Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu
 100 105 110

Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
 115 120 125

Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
 130 135 140

Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr
 145 150 155 160

Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe
 165 170 175

Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val Lys
 180 185 190

Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile Met Val Lys Asp Asn
195 200 205

Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser Arg
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Val Lys Pro Asp Pro Pro His Ile Lys Asn Leu Ser Phe His Asn Asp
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Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln Thr Glu Thr His Asn
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Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg
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Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro Asp
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Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr
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Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile Gly
325 330 335

Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val Pro
340 345 350

Val Ile Val Ala Gly Ala Ile Ile Val Leu Leu Leu Tyr Leu Lys Arg
355 360 365

Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
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Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
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Tyr Asp Ile Tyr Glu Lys Gln Thr Lys Glu Glu Thr Asp Ser Val Val
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Glu Val Gln Pro Pro Val Thr Xaa Leu Ser Val
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Glu Val Gln Pro Pro Val Thr Xaa Leu Ser Val
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